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Detection of multiple potential alternative hosts of begomoviruses in Madagascar, using multiplexed parallel amplicon pyrosequencing

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In the last decades, begomoviruses emerged as probably the most economically important crop pathogens. Despites the hypothesis that uncultivated hosts, such as wild plants or weeds, provide alternative hosts during intercropping periods, few studies effectively identified the plant species involved. Here, we used multiple parallel-sequencing of a conserved region of begomovirus genome, using newly designed primers, to identify the presence of begomoviruses in a large number of wild plants and crops in Madagascar and sub-Saharan African countries. Whereas our primers set successfully amplified begomoviruses in a wide range of plant species and families, we focused our analyses on Madagascan samples, and identified four distinct Operational Taxonomic Units (OTUs), that infect both crop and weeds. While one of these OTUs likely represents an example of a malvaceous-adapted virus which acquired the ability to infect bean, three closely related OTUs, largely prevalent on tomato, were found infecting weeds. One of these tomato-associated OTU in particular, related to variants of tomato leaf curl Madagascar virus, was found in eight distinct plant species, suggesting its evolution as a generalist pathogen. Despites several biases associated to the use of primers designed from known sequences, and the need to confirm our results with the cloning of complete sequences, our study has unravelled the complexity of the relationships between begomoviruses and their hosts and raised some exciting questions on the niche partitioning of begomoviruses in natural and cultivated ecosystems.

Mots-clés : Begomoviruses; Madagascar; Host range; Pyrosequencing.